

# DIVERSITY OF YIELD COMPONENT TRAITS IN SEVERAL GENOTYPES OF SWEET CORN

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## Abstract

Sweet corn is a type of corn that has been widely cultivated in Indonesia. It is preferred over regular corn due to its sweeter taste. The increase in sweet corn production can be achieved by expanding the planting area or using high-yielding varieties. In plant breeding, the focus on increasing crop production is primarily through the use of high-yielding varieties. One approach is through plant selection, where high-yielding potential plants are selected to become superior varieties. At the initial stage of selection from crosses, plants with wide genetic diversity are identified. The selected plants are then developed to become more uniform, indicated by a narrower range of diversity. Narrow genetic diversity is achieved in advanced generations. The aim of this study was to examine the genetic diversity and trait feasibility in the developing lines of sweet corn as a basis for further selection. The materials used in the study were 14 lines of sweet corn, fertilizers, and pesticides. Sweet corn was planted in plot land using a Randomized Block Design with two replications. The results from the fourth generation of sweet corn plants showed that the traits of leaf number, plant height, ear length, and husk length exhibited narrow genetic diversity in most populations. Traits with narrow genetic diversity in the plant population can be selected again to increase uniformity and homozygosity in subsequent generations, leading to a fully uniform population.

**Keywords:** genetic diversity, uniformity, sweet corn, selection.

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## 1. INTRODUCTION

Sweet corn is a member of the Poaceae family. It is reported to be a mutant of field corn, characterized by possessing at least one of eight mutant genes [1]. Sweet corn is one of the most widely cultivated crops in Indonesia, primarily used as food, both for fresh consumption and as raw material or processed products in the food industry [2]. In sweet corn, sweetness is influenced by the amount of sugar and starch in the endosperm [3]. Sweetness is not only determined by genetics but also by handling and harvesting methods for each variety. Sivamurugan et al. [4] also stated that crop management plays a crucial role in achieving sweetness in the cobs, in addition to the genetic composition.

The potential for sweet corn development in Indonesia is promising, given the increasing demand for food. Therefore, the availability of food needs to be increased to meet the rising demand for sweet corn. Using high-yielding varieties can be an alternative solution, aside from expanding the cultivation area. Corn yield is one of the most important and complex quantitative traits, controlled by many genes [5]. The development of high-yielding varieties can be achieved through plant breeding activities.

Plant breeding methods that have been known and practiced for centuries include selection [6]. Plant selection is done by choosing and taking planting material from existing plants with desirable traits. Two factors that determine the success of selection are the value of diversity and

heritability. The diversity value indicates the extent of variation present within the plant population. A good diversity value as a source for selection is one that shows a wide range of variation. According to Dagnaw et al. [7], genetic variability for agronomic traits is a key component of breeding programs to expand the gene pool of plants. High plant diversity can increase the response to plant selection. Heritability is an indicator of the extent to which a trait is influenced by genetic or environmental factors [8]. High heritability in plants can facilitate selection by indicating the progress of selection based on the estimated heritability value. According to Young et al. [9], it is important to know the estimated heritability value of a trait to predict the progress of selection and to determine whether the trait is more influenced by genetic or environmental factors. Heritability in the broad sense is the proportion of genetic variance relative to phenotypic variance. The greater the heritability value, the greater the selection progress achieved, and the faster superior varieties can be released [10].

Plant traits can be classified into two categories: qualitative and quantitative traits. Qualitative traits refer to characteristics that can be observed in terms of presence or absence, without being measured for degree or value. Quantitative traits, on the other hand, are measurable in terms of value or degree [11]. Quantitative traits in plants reflect the production quantity through the phenotypic traits displayed.

## 2. MATERIALS AND METHODS

The experiment was conducted in Bangladesh Agriculture University. The materials used were 14 lines of sweet corn. The insecticide used had an active ingredient of profenofos 500g/l, and the fungicide contained pyraclostrobin 250g/l. Other materials included organic fertilizer, NPK fertilizer, SP-36, and KCl.

The experimental design used in this study was a Randomized Block Design (RBD) with 14 treatments (14 lines of sweet corn). The experiment began with land preparation, followed

by planting, maintenance, harvesting, and observation. The observed parameters were quantitative plant traits. The quantitative traits observed included plant height, number of leaves, ear placement, ear height, ear length, ear stalk length, number of rows, and husk length.

The broad-sense heritability estimate ( $h^2$ ) was calculated using the following formula:

$$h^2 = \frac{\sigma^2_G}{\sigma^2_P}$$

where:

- $h^2$  = estimated broad-sense heritability
- $\sigma^2_G$  = genetic variance
- $\sigma^2_P$  = phenotypic variance

According to Stansfield in Boer (2011), the criteria for heritability estimates ( $h^2$ ) are as follows:

- High if  $h^2 > 0.50$
- Medium if  $0.20 \leq h^2 \leq 0.50$
- Low if  $h^2 < 0.20$

## 3. RESULTS AND DISCUSSION

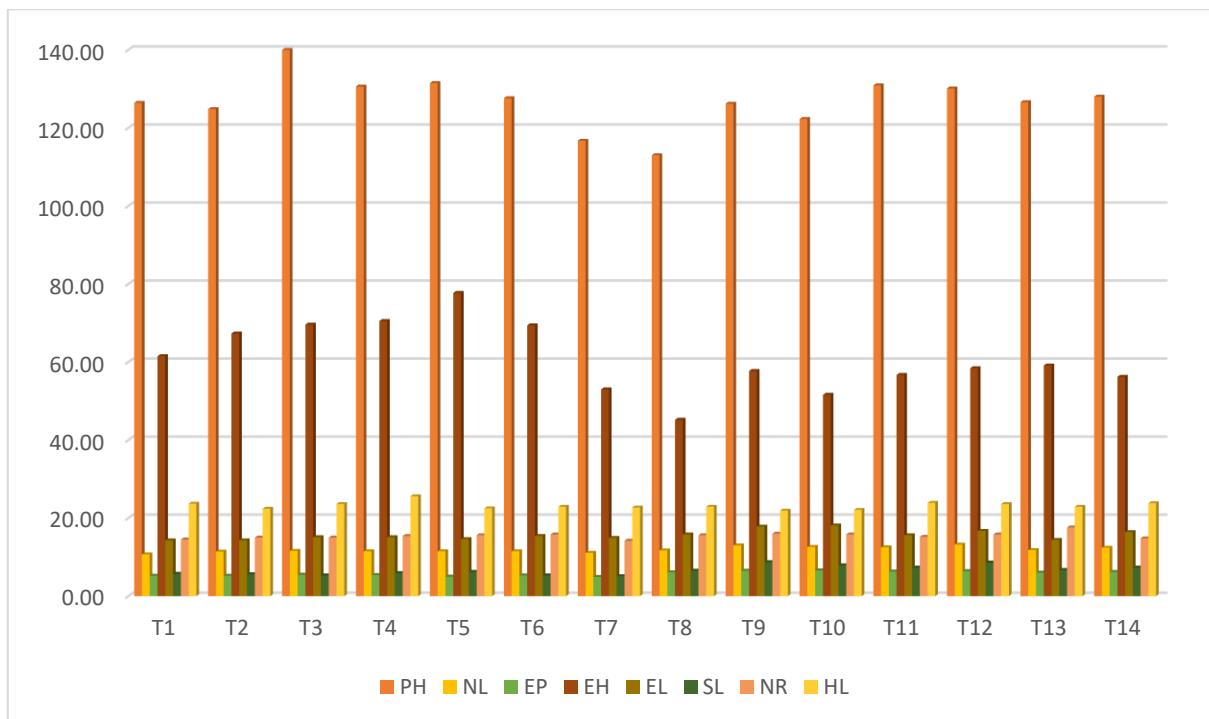
Variance data describes the distribution of data within a quantitative dataset. The analysis of variance results in Table 1 show that most of the observed traits exhibit significant differences, except for the number of rows and husk length.

This indicates that different treatments applied to the fourteen populations of self-pollinated sweet corn had a significant impact on most of the plant characteristics, except for the number of rows and the length of the husk. The results of the Duncan's 5% test (Figure 1) show that the different population treatments led to a significant difference in plant height between population T8, which had the smallest average height, and population T3, which had the largest average height. Population T8, as the smallest average, was not significantly different from population T7.

**Table 1. Analysis of Variance Results for Sweet Corn Traits**

Trait	Mean	Mean Square	F Value
Plant Height	126.78	85.9	7.22*
Number of Leaves	11.9	1.1	2.75*
Ear Placement	5.76	0.7	3.5*
Ear Height	61.02	156.6	4.08*
Ear Length	15.63	3.1	6.2*
Stalk Length	6.6	2.9	3.2*
Number of Rows	15.46	1.4	1.17 <sup>NS</sup>
Husk Length	23.2	1.8	1.13 <sup>NS</sup>

**Note:** \* = significant at 0.05 level; NS = not significant at 0.05 level.



**Figure 1. Average Values for Plant Height, Number of Leaves, Ear Placement, Ear Height, Ear Length, Stalk Length, Number of Rows, and Husk Length (Note: PH = Plant Height, NL = Number of Leaves, EP = Ear Placement, EH = Ear Height, EL = Ear Length, SL = Stalk Length, NR = Number of Rows, HL = Husk Length).**

For the leaf number trait, a significant difference was observed between population T1 and T12, with T12 having the highest average number of leaves. The leaf count in population T1 was not significantly different from 8 other populations, namely T2, T3, T4, T5, T6, T7, T8, and T13.

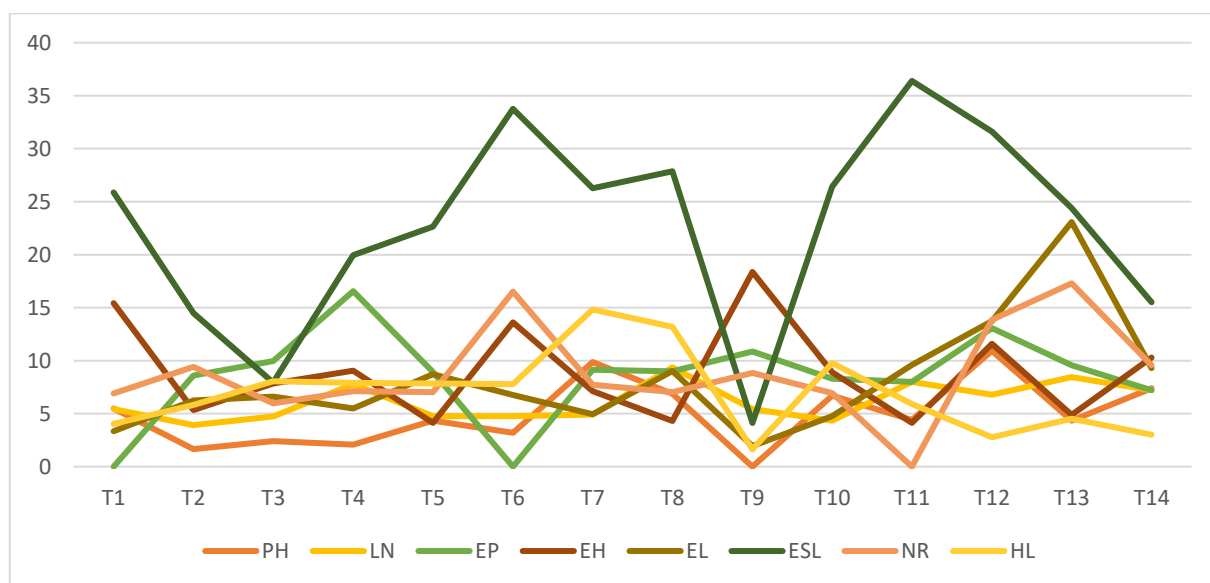
In terms of the ear placement, a significant difference was found between population T7 and

T10. Population T7, with the smallest average, was not significantly different from six other populations, from T1 to T6. In the ear height trait, population T8 had the smallest average at 45.2, which was not significantly different from populations T7, T9, T10, T11, T12, and T14. However, it showed significant differences from populations T1, T2, T3, T4, T5, T6, and T13.

The average values of populations T1 and T2 were the same at 14.3, the smallest for the ear length trait. These two populations were not significantly different from populations T3, T4, T5, T6, T7, T8, T11, and T13. All of these populations were significantly different from populations T9 and T10, which had average ear lengths of 17.8 and 18.1. Population T7 had the smallest average for ear stalk length and was not significantly different from populations T1, T2, T3, T4, T5, T6, T8, and T13. A significant difference was observed between population T7 and T9, which had the largest average, as well as between T10 and T14, except for T13.

The number of rows and husk length traits did not show significant differences among the populations. The notation shown in the average of each population indicates that the smallest value of each population's trait was not significantly different from twelve other populations. Differences in notation were only seen between the largest and smallest values for each trait.

In most sweet corn traits, there were significant differences among populations. These differences in plant growth were influenced by both genetic and environmental factors [12].



**Figure 2: Coefficients of Genetic Variation for Plant Height, Leaf Number, Ear Placement, Ear Height, Ear Length, Ear Stalk Length, Number of Rows, and Husk Length (Note: PH= Plant Height, LN= Leaf Number, EP= Ear Placement, EH= Ear Height, EL= Ear Length, ESL= Ear Stalk Length, NR= Number of Rows, HL= Husk Length).**

Different genotypes will exhibit distinct characteristics when interacting with their environment. This suggests that genetic variability provides a rich source of material for selection activities.

The genetic variability coefficient values in Figure 2 show that the plant height trait in thirteen populations has a low genetic variability, while one population, T12, has a moderate coefficient of 10.93%. A low genetic variability coefficient indicates that plant height has a narrow genetic diversity.

In the leaf count trait, all populations show narrow genetic diversity. This narrow genetic diversity suggests that the number of leaves is already quite uniform, indicating that the selection process for obtaining homozygous plants is nearing completion. Three populations—T4, T9, and T12—show moderate genetic variability for the ear placement trait. Populations with moderate variability will require more time to achieve uniformity compared to populations with low variability. The other eleven populations with low genetic variability can be selected for the next period as they will achieve uniformity in a shorter time.

The highest coefficient of genetic variability for ear height is 18.37%, found in population T9. Other populations with moderate variability include T1, T6, T12, and T14, while the rest have low variability. For ear length, population T12 shows moderate variability, and T13 has high variability with coefficients of 13.74% and 23.08%, respectively. Population T13's high coefficient indicates wide genetic variability. Other populations exhibit narrow variability.

The stalk length trait shows narrow genetic variability in populations T3 and T9, with coefficients of 7.93% and 4.12%, respectively. Three populations—T2, T4, and T14—have moderate variability, while nine other populations (T1, T5, T6, T7, T8, T10, T11, T12, and T13) show high genetic variability. Most of the populations in the fourth generation are not suitable for further development as planting material based on stalk length due to high variability. High variability will require more time to achieve uniform, homozygous plants.

For the row number trait, most populations show narrow genetic variability. Populations with narrow genetic variability include T1, T2, T3, T4, T5, T7, T8, T9, T10, T11, and T14. As these populations have narrow variability, achieving uniform plants for row number will take less time. Populations T6, T12, and T13 show moderate variability for this trait.

The husk length trait shows that most populations have narrow variability, except for populations T7 and T8, which show moderate variability with coefficients of 14.83% and 13.18%, respectively.

The genetic variability values in each maize population can be used as a consideration for selecting which population can be used as planting material for the next season. In addition to genetic variability, heritability should also be considered when selecting plants. Populations with narrow genetic variability are preferred for the next planting season because achieving uniformity in subsequent generations will be faster. The selfing effect can cause greater uniformity or homozygosity compared to the previous population [13]. However, continued

selfing can negatively affect plant vigor and desirable traits.

Table 2 shows the heritability estimates, indicating whether traits are more influenced by genetic or environmental factors. For plant height, high heritability is observed in populations T1, T3, T4, T5, T6, T7, T10, T11, T12, and T14. Three other populations, T2, T8, and T13, have moderate heritability. These ten maize populations with high heritability indicate that the plant height trait is more influenced by genetic factors than environmental factors.

For the leaf count trait, all populations show high broad-sense heritability. The lowest heritability value for this trait is found in population T1, with a value of 0.54, indicating that genetic factors largely influence the leaf count in the fourth selfing generation.

For the ear placement trait, two populations, T1 and T6, show low heritability, while twelve other populations exhibit high heritability. This indicates that genetic factors primarily influence most populations, while two populations are more influenced by environmental factors.

The smallest heritability estimate for ear height is 0.21, found in population T11, placing it in the moderate heritability category. Four maize populations (T2, T3, T8, and T11) fall within the moderate heritability range, while ten other populations exhibit high heritability.

For ear length, three populations—T1, T9, and T10—have moderate heritability, with values of 0.36, 0.23, and 0.50, respectively. Other populations have high heritability, with the highest value in population T7. One population, T9, shows low heritability for stalk length, with a value of 0.13. Two other populations, T3 and T12, show moderate heritability, while eleven other populations exhibit high heritability. The highest heritability for stalk length is found in population T4, with a value of 0.98.

For the row number trait, population T11 shows low heritability, while population T10 has moderate heritability with a value of 0.48. The low heritability in these two populations suggests

that the row number trait is more influenced by environmental factors than genetic ones. Twelve other maize populations for the row number trait have high heritability, indicating that the trait is largely controlled by genetic factors.

For the husk length trait, four populations—T9, T11, T12, and T14—have moderate heritability, while ten other populations have high heritability. The highest heritability for husk length is found in population T7, with a value of 0.98.

Heritability values can be used to assist in selecting which populations can be used to improve the uniformity of plants for specific traits. Populations with high heritability values for established traits are preferred for the next planting season. Plants in subsequent generations will have a greater chance of exhibiting similar traits to the previous generation because the expression of these traits is more influenced by genetic factors. According to Abikkumar et al. [12], traits with high heritability have a greater role of genetic factors compared to environmental factors in determining a phenotype and have a

higher likelihood of being inherited by the offspring.

Figure 3 shows the correlations between each plant trait. The correlations between traits can be either positive or negative. Positive values indicate a direct relationship between traits, while negative values indicate an inverse relationship. From Figure 3, it is evident that plant height has a strong positive correlation with ear height. Li et al. [14] found a similar correlation, with plant height and ear height having a strong relationship. The correlation value between plant height and ear height is 0.71, indicating a close relationship between these traits. This means that as plant height increases, the ear height will also increase. The positive correlation between plant height and ear height can be considered in plant improvement [15]. The number of leaves has a strong correlation with ear placement, ear length, and stalk length. This suggests that a greater number of leaves can increase plant production, as the number of leaves is strongly correlated with ear length. Ear placement shows a strong correlation with both ear length and stalk length.

**Table 2: Heritability Estimates for Plant Height, Number of Leaves, Ear Placement, Ear Height, Ear Length, Stalk Length, Row Number, and Husk Length**

Population	Plant Height (TT)	Number of Leaves (JD)	Ear Placement (LTo)	Ear Height (TTo)	Ear Length (PTo)	Stalk Length (PtaTo)	Row Number (JBB)	Husk Length (PK)
T1	0.68	0.54	0.00	1.00	0.36	0.93	1.00	0.76
T2	0.44	0.58	0.89	0.38	0.64	0.73	0.71	0.59
T3	0.69	0.74	0.74	0.40	0.71	0.43	0.67	0.75
T4	0.56	1.00	1.00	0.81	0.77	0.98	0.68	0.66
T5	0.73	1.00	1.00	0.69	0.81	0.73	0.63	0.56
T6	0.62	0.74	0.00	0.89	0.75	0.80	0.90	0.70
T7	0.92	0.63	0.90	0.51	0.99	0.85	0.77	0.98
T8	0.43	0.84	0.55	0.25	0.73	0.85	0.68	0.96
T9	0.00	1.00	1.00	0.91	0.23	0.13	1.00	0.45

Population	Plant Height (TT)	Number of Leaves (JD)	Ear Placement (LTo)	Ear Height (TTo)	Ear Length (PTo)	Stalk Length (PtaTo)	Row Number (JBB)	Husk Length (PK)
T10	0.94	0.78	0.74	0.73	0.50	0.96	0.48	0.93
T11	0.75	1.00	0.66	0.21	0.84	0.72	0.00	0.46
T12	0.95	0.68	0.80	0.83	0.75	0.44	0.87	0.35
T13	0.47	0.92	1.00	0.53	0.84	0.85	0.94	0.79
T14	0.95	0.89	0.67	0.90	0.79	0.82	0.61	0.40

**Note:** TT = Plant Height, JD = Number of Leaves, LTo = Ear Placement, TTo = Ear Height, PTo = Ear Length, PtaTo = Stalk Length, JBB = Row Number, PK = Husk Length

Trait	TT	JD	LTo	TTo	PTo	PtaTo	JBB	PK
TT	1	0.13	-0.06	0.71	-0.13	-0.01	0.06	0.41
JD		1	0.88	-0.35	0.82	0.93	0.38	-0.14
LTo			1	-0.6	0.81	0.89	0.43	-0.11
TTo				1	-0.5	-0.43	-0.01	0.23
PTo					1	0.81	0.16	-0.29
PtaTo						1	0.4	-0.19
JBB							1	-0.2
PK								1

**Figure 3: Correlation Between Sweet Corn Plant Traits** (Note: TT = Plant Height, JD = Number of Leaves, LTo = Ear Placement, TTo = Ear Height, PTo = Ear Length, PtaTo = Stalk Length, JBB = Row Number, PK = Husk Length).

The correlation values between the two traits are 0.81 and 0.89, respectively. A negative correlation is observed between ear placement and ear height, with a value of -0.60. According to Nemati et al. [16], this negative correlation is classified as moderate.

#### 4. CONCLUSION

In advanced generations of plants, narrow variability in specific traits is required to achieve uniformity. Traits such as plant height, number of leaves, ear placement, ear length, and row number in most populations show narrow genetic variability. Populations with narrow genetic variability and high heritability estimates for specific traits should be selected for the next planting period. Achieving uniformity in plant traits in advanced generations is the goal of plant

selection activities. The time needed to reach uniform and homozygous plants will be shorter with narrow genetic variability and high heritability estimates for the plant traits.

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